

Lesson 11:

Entering TBCF Records

In this lesson you'll learn about the following:

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Introduction to the VS TB Disease Program

USDA:APHIS:VS is involved in eradicating the Tuberculosis (TB) disease from the bovine, captive and wild bison, deer, and elk species (and others) living in the United States of America. This infectious disease is spread primarily by a healthy animal either inhaling or ingesting infected droplets coughed or expelled from an infected animal. Because TB bacteria can survive for up to two months in a pasture after a sick animal first expels them, this disease can spread quickly throughout a herd. TB can progress fast or slowly in an animal, usually manifests as lesions on the animal's body, and currently cannot be treated successfully.

As of 2003, the accepted method for diagnosing and eliminating TB in animals is a combination of surveying slaughtered animals for any evidence of infection and performing skin tests on live animals. For both approaches, all tests and procedures must adhere to the standards set forth in the USDA's *Bovine Tuberculosis Eradication Uniform Methods and Rules* (UM&R) document, last issued on January 22, 1999. But, in general, the following principles and procedures apply.

Surveillance of Slaughter Animals

An animal found infected after being slaughtered is traced to the farm or ranch of origin (where the animal was born). The optimum method of eliminating TB on the premises-of-origin is to depopulate all cattle and other susceptible species, such as other ruminants (sheep, deer, etc.), dogs, cats, horses, and swine.

Live-Animal Skin Testing

An alternative to depopulation is to perform live-animal skin tests on all the cattle at the premises-of-origin in order to find other infected animals to send to immediate slaughter. Any other premises associated by contact, sales, or purchases should also have all their cattle skin-tested to determine whether TB is present in their herds.

For live cattle, there are two primary diagnostic tests used to detect TB:

1. The TB CF (caudal fold) skin testing procedure consists of injecting bovine tuberculin into the skin of the caudal fold (the loose skin at the base of the animal's tail). This injected site is re-examined 72 hours later to see if there is any response (such as swelling of the skin). An animal that exhibits a response to the TB CF test is called a *responder* animal.

This animal is then more specifically classified as either a *suspect* animal or a *reactor* animal, depending on the initial status of the herd the animal comes from:

- If the herd has a known status (such as *infected* or *quarantined*), the responder animal is more specifically classified as a reactor animal. Reactor animals are removed from the herd within 15 days of identification.
 - If the herd has an unknown status, the responder animal is classified as a suspect animal. A suspect animal is either re-tested with the TB comparative cervical test (TB CC) or sent to immediate slaughter.
2. The TB CC (comparative cervical) testing procedure is used to differentiate between a reaction to bovine mycobacterial infection (TB) and exposure to soil-borne mycobacteria (avian TB). The TB CC test is accomplished by simultaneously injecting both bovine and avian tuberculin in two places on a shaved area of the animal's neck. This injected site is re-examined 72 hours later for any reactions. The tested animal will be classified as a suspect if it reacted more strongly to the bovine tuberculin or as a reactor if it reacted more strongly to the avian tuberculin.

For live captive and wild bison, deer, and elk species, a third TB diagnostic test is used. This TB SC (single cervical) testing procedure is done only on selected animals under special circumstances (such as belonging to a known infected elk or deer herd where depopulation and repopulation is not an option). Similar to the TB CF test, the bovine tuberculin is injected into the animal's neck. The results of this test will classify an animal as either a negative or a reactor.

Exercise 1: Entering TBCF Summary Data

- 1.1 Access a new, blank **TBCF Event_Summary** form by doing the following steps:
- From the **APHIS IMMS** main menu, click on the **Generic Data Base** option.
 - In the **Generic Data Base** menu, click on the **Forms** option.
 - In the **Forms** menu, click on the **GDBTBCF: TBCF Test** option.

A new **TBCF Event_Summary** form will appear onscreen.

The screenshot shows a software window titled "devlco-GDBTBCF" with a menu bar (Action, Edit, Query, Block, Record, Field, Window, Help). The form is divided into two main sections:

PREMISES QUERY

Prem ID: Prem Name:
 Address:
 Prem Type/Species: City: State:
 Zip: County:
 County Name:

EVENT SUMMARY INFORMATION

Prem ID: Disease: Entry Date:
 Prem State: Species: V Entry State:
 Prem Type: Event Type: V Event County:
 Es Nr: Event Seq Nr:

Area	ARE	Retest	RT
Herd(Re)	HA	Tracing	TK
Accredit	HA	Reg Kill	TK
Milk	MO	Tracing	TR
Ordinance	MO	Reactors	TR
Sale Show	SS	Tracing	TE
Exposed	SS	Exposed	TE
Imported	IMP	Other	OTH

Rsn for Test: V Nr Neg: Paycode: V
 Nr in Lot: Nr Dev (Sus): Person ID: L
 Kind: Nr Rea: Person State: L
 Injec Site: L Nr Oth: Injec Date:
 Total: Read Date:

Serial Nr A: Pay Stop: Lab: L User Field 1: L
 Serial Nr B: Fund: Lab State: L User Field 2: L
 Nr No Test: Event3 Date: User Field 3: L
 Remarks:

Buttons: Sample, Short Sample, Status, Misc Info, New, Clear, Save, Exit
 Premises, Person

The cursor will be in the **Prem ID** field of the *Premises Query* block. The form will be in data-retrieval mode.

- 1.2 Query the premises at which the event occurred by entering a **Prem ID** and pressing **F8**. If a premises is found, the cursor will move to the **Rsn for Test** field of the *Event Summary Information* block.

- 1.3 Verify that the **Prem Type** and **Species** in the *Event Summary Information* block match the **Prem Type** and **Species** in the *Premises Query* block (as shown by the dark lines in the screen image below).

The screenshot displays two main sections: **PREMISES QUERY** and **EVENT SUMMARY INFORMATION**.

PREMISES QUERY fields include:

- Prem ID: C0555011
- Prem Name: Shulton Enterprises
- Address: 1340 Blakesville End
- City: Rustic
- State: CO
- Zip: 80444
- County: 069
- County Name: Larimer
- Prem Type/Species: BRD BOV (with a dropdown arrow)

EVENT SUMMARY INFORMATION fields include:

- Prem ID: C0555011
- Prem State: CO
- Prem Type: BRD
- Es Nr: 20023571861
- Disease: TB
- Species: BOV (with a checkmark)
- Event Type: TBCF (with a checkmark)
- Event Seq Nr: 0
- Entry Date: 23-DEC-2002
- Entry State: GA
- Event County: 069

Dark lines indicate the comparison between the **Prem Type/Species** field in the **PREMISES QUERY** block and the **Prem Type** and **Species** fields in the **EVENT SUMMARY INFORMATION** block.

If they do not match for the test to be entered, do the following:

- Click to place the cursor in the *Prem Type/Species* sub-block of the *Premises Query* block.
- Use the UP ARROW and DOWN ARROW keys in the sub-block to scroll through the **Prem Type/Species** records to find the correct combination.
- After you have found the correct combination, press CTRL+PAGE DOWN to return to the *Event Summary Information* block. The cursor will move to the **Rsn for Test** field.

If you cannot find the correct **Prem Type** and **Species** in the *Event Summary Information* block, it may mean that a **Premises_Supplemental Record** has not yet been created for this combination. To create this missing record:

- Return to *Lesson 3: Entering Herd Test Records* in this manual.
- Query for and retrieve the **Premises Record** that has this **Prem ID**.
- Create the missing **Premises_Supplemental Record** by doing Steps 2.28 through 2.39 in Lesson 3.
- Then come back to this Lesson 11 and continue with Step 1.4 below.

- 1.4 In the **Rsn for Test** field, enter the appropriate value. Press ENTER.

- 1.5 **Nr in Lot** is not a required field. Enter data or not, as desired. Press ENTER.

Note: The **Kind** field does not allow you to enter data into it. The information displayed in this field is intended simply to show the relationship to the fields of the VS 6-22 form.

- 1.6 **Injec Site** is not a required field. A value of **CFLS** appears in this field, because it is the default value for any **Event_Summary Record** whose **Event Type=TBCF**. You can accept this default value or change it. Then press ENTER.

- 1.7 In the following four fields, you can enter a new value or accept **0** as the default value. Press ENTER to move between fields.

Nr Neg

Nr Dev (Sus)

Nr Rea

Nr Oth

- 1.8 In the **Paycode** field, enter the appropriate value. Press ENTER.

- 1.9 **Person ID** and **Person State** are not required fields. Enter data or not, as desired. Press ENTER.

- 1.10 In the **Injec Date** field, enter the appropriate date, using the format of dd-MON-yyyy (for example, **04-AUG-2003**). Press ENTER.

- 1.11 The **Read Date** is not a required field, but it defaults to three days after the **Injec Date** value. You can accept this default value or enter a different **Read Date** value. (If you change this value, use the format, dd-MON-yyyy).

At this point, you have finished entering the minimal data required for this **TBCF Event_Summary** form. Below is an example of what your form might look like:

PREMISES QUERY			
Prem ID:	C0555011	Prem Name:	Shulton Enterprises
		Address:	1340 Blakesville End
Prem Type/Species		City:	Rustic
BRD	BOV	State:	CO
		Zip:	80444
		County:	069
		County Name:	Larimer

EVENT SUMMARY INFORMATION			
Prem ID:	C0555011	Disease:	TB
Prem State:	CO	Species:	BOV
Prem Type:	BRD	Event Type:	TBCF
Es Nr:	20023571861	Event Seq Nr:	0
		Entry Date:	23-DEC-2002
		Entry State:	GA
		Event County:	069

Area	ARE	Retest	RT	Rsn for Test:	HQ	Nr Neg:	0	Paycode:	4
Herd(Re)	HR	Tracing	TK	Nr in Lot:		Nr Dev (Sus):	0	Person ID:	
Accredit	HA	Reg Kill	TK	Kind:		Nr Rea:	0	Person State:	
Milk	MO	Tracing	TR	Injec Site:	CFLS	Nr Oth:	0	Injec Date:	04-OCT-2002
Ordinance	HO	Reactors	TR			Total:	0	Read Date:	07-OCT-2002
Sale Show	SS	Tracing	TE						
Exposed	ES	Exposed	TE						
Imported	IHP	Other	OTH						

Serial Nr A:		Pay Stop:		Lab:		User Field 1:	
Serial Nr B:		Fund:		Lab State:	GA	User Field 2:	
Nr No Test:				Event3 Date:		User Field 3:	
Remarks:							

Sample	Short Sample	Status	Misc Info	New	Clear	Save	Exit
Premises	Person						

1.12 You can now do any of the following:

To Start This Task...	Do This Action
Enter more data on this TBCF Event_Summary form...	<ol style="list-style-type: none"> 1. Click inside specific fields to enter data into them. 2. After you have entered all of your data, press F10 to re-commit this TBCF Event_Summary Record back into the GDB.
Create Sample Records for individual animals...	Go directly to <i>Exercise 2: Entering TBCF Sample Data</i> in this lesson.
Exit this form (because you have finished all of your data-entry work)...	Click the [Exit] command button. You have now finished this Exercise 1.

Exercise 2: Entering TBCF Sample Data

In this exercise, you have a choice of entering detailed TBCF sample data using a **TBCF** full-size **Sample** form or entering minimal sample data by using a **TBCF** short **Sample** form. Read these next two pages to help you decide which form you wish to use.

Below is a new **TBCF** full-size **Sample** form:

SUMMARY INFORMATION									
TB Nr: 20023571861		Prem Id: C0555011		Prem State: CO		Species: BOV		Event Type: TBCF	
Entry State: GA		Disease: TB							
SAMPLE INFORMATION									
TB Seq Nr: 1		Eartag(Id1):		Id1 Source: L		Age:		Test Interp: N L	
Bngl/Btg(Id2):		Id2 Source: L		Breed: L		Nr Neg:		Nr Sus:	
		Tag Query		Sex: L		Nr Pos:			
Ind Range:		Id3:		Pay Group:		Origin:		Q	
Unit:		Id4:		Ind Id:		Origin State:			
Nr In Lot:		Tat:		Case Nr:		Prem Name:			
		Id6:				Disposition:			
OWNER INFORMATION									
Prem Id: Q									
Owner Name:									
Owner City:		Owner State:							
Owner Country:		County Name:							
Remarks:									
Test Name:									
Test Result:									
Summary		New		Clear		Save		Exit	

And below is a new **TBCF** short **Sample** form:

SUMMARY INFORMATION														
ES NR	ST	Dis	Spe	Type	Date	Rsn	Seq NR							
20023571861	GA	TB	BOV	TBCF	04-OCT-2002	HQ	0							
Prem ID: C0555011		Prem Name: Shulton Enterprises			Prem State: CO									
SAMPLE INFORMATION														
Seq NR	I/R	Unit	NR in Lot	NR Neg	NR Sus	NR Pos	ID1 - Eartag	ID2 - Backtag	ID5 - Vac	TI	Age	BR	Sex	Pay Grp
1										N				
Species: BOV		Tag Query		Origin: Q										
				Origin State:										
				Prem Name:										
TEST INFORMATION														
Sample Seq NR:														
Test Name:														
Test Result:														
Summary		New		Clear		Save		Exit						

The differences between the full-size **Sample** form and the short **Sample** form are listed below:

Full-Size Sample Form	Short Sample Form
Has six ID fields to describe one animal or group of animals: Eartag (Id1) Bngl/Btg (Id2) Id3 Id4 Tat Id6	Has three ID fields to describe one animal or group of animals: ID1-Eartag ID2-Backtag ID5-Vac (vaccination number)
Uses the entire <i>Sample Information</i> block of the Sample form to describe one animal or group of animals.	Uses a single row of fields (from the Seq NR field through the Pay Grp field) as a record to describe a single animal or group of animals.
Allows you to create only one TBCF Sample Record on the full-size Sample form.	Allows you to create/display up to five TBCF Sample Records at one time on the short Sample form. (The form will scroll to allow you to display or enter additional Sample Records .)

The next two sub-sections will teach you how to do the following tasks:

Exercise 2A Create a **TBCF Sample Record** using the full-size **Sample** form

Exercise 2B Create one or more **TBCF Sample Records** using the short **Sample** form

Note: Creation of a **Sample Record** may not be required if the animal's test result is negative. However, if the animal is other than negative, a **Sample Record** may be created for traceback purposes.

Exercise 2A: Using the Full-Size Sample Form

In this exercise, you will learn how to do enter TBCF animal sample data and test results data on a full-size **Sample** form.

2A.1 The cursor should still be inside any field in the *Event Summary Information* block of your **TBCF Event_Summary** form. At the bottom of the form, either:

- click the [Sample] button
- press CTRL+PAGE DOWN

The **TBCF** full-size **Sample** form will appear:

The screenshot shows the GDBTBCF SUMMARY INFORMATION and SAMPLE INFORMATION form. The SUMMARY INFORMATION section includes fields for TB Nr (20023571861), Prem Id (C0555011), Entry State (GA), Disease (TB), Prem State (CO), Species (BOV), and Event Type (TBCF). The SAMPLE INFORMATION section includes fields for TB Seq Nr (1), Eartag (Id1), Bngl/Btg (Id2), Id1 Source, Id2 Source, Age, Breed, Sex, Test Interp (N), Nr Neg, Nr Sus, Nr Pos, Ind Range, Unit, Nr In Lot, Id3, Id4, Id6, Pay Group, Ind Id, Case Nr, Origin, Origin State, Prem Name, Disposition, User Field 1, User Field 2, User Field 3, Prem Id, Owner Name, Owner City, Owner State, Owner Country, County Name, Remarks, Test Name, and Test Result. The form has a Summary button at the bottom left and New, Clear, Save, and Exit buttons at the bottom right.

2A.2 The cursor will be in the **TB Seq Nr** field. Do one of the following:

- Press ENTER to accept the default value.
- Change the sequence number. Press ENTER.

2A.3 In the **Eartag (Id1)** field, enter the eartag number, if available. Press ENTER.

- 2A.4 In the **Bngl/Btg (Id2)** field, enter the bangle or back tag number, if available.
Press ENTER.

Origin:	C0555011	Q
Origin State:	CO	
Prem Name:	Shulton Enterprises	
Disposition:		

- 2A.5 Pressing the [Tag Query] button will cause the GDB to query its **Miscellaneous_Information Table** to find **Prem IDs** for those premises to which tags were initially distributed.

(In order for this [Tag Query] button to work, the tag distribution information must already exist in the GDB's **Miscellaneous_Information Table**.)

- Any records retrieved will appear on a **Tag Distribution** form.
 - You would select the appropriate **Prem ID** from those shown on the **Tag Distribution** form.
 - The **Prem ID** you select will be inserted into the **Origin** field of the **TBCF Sample** form.
- 2A.6 In the **Age** field, enter the age of the animal tested, if available. Press ENTER.
- 2A.7 In the **Breed** field, enter the breed, if available. Press ENTER.
- 2A.8 In the **Sex** field, enter the animal's sex, if available. Press ENTER.
- 2A.9 In the **Test Interp** field, enter a new value or accept **N** (negative) as the default value.

Note: To bypass the **Nr Neg**, **Nr Sus**, and **Nr Pos** fields when the cursor is in the **Test Interp** field, press the **F5** hot key. The cursor will move to the **Ind Range** field. However, if you press ENTER when the cursor is in the **Test Interp** field, the cursor will move to the **Nr Neg** field.

- 2A.10 If an animal came from another premises to the current premises, you can specify the original premises in the **Origin** sub-block.

Enter a **Prem ID** value in the **Origin** field and press the **Q** button next to it.

A query will be executed against the GDB's **Premises Table**. If the **Prem ID** value in the **Origin** field matches a **Prem ID** in the **Premises Table**, the name of the premises that has this **Prem ID** will be displayed in the **Prem Name** field.

2A.11 In the **Ind Range** field, enter one of the following values:

I to represent one animal

R to represent several animals

Press ENTER.

2A.12 In the **Nr in Lot** field, enter the appropriate number, if available. Press ENTER.

2A.13 In the **Unit** field, enter the appropriate value, if available. Press ENTER.

In most cases, your data-entry work in the **TBCF** full-size **Sample** form will end at the **Unit** field (if not earlier).

Your **TBCF** full-size **Sample** form should now look similar to the example below:

SUMMARY INFORMATION			
TB Nr: 20023571861	Prem Id: C0555011	Prem State: CO	
Entry State: GA	Disease: TB	Species: BOV	
		Event Type: TBCF	

SAMPLE INFORMATION			
TB Seq Nr: 1	Age: 4	Test Interp: N	
Eartag(Id1): HJDM7209	Id1 Source: L	Nr Neg:	
Bngl/Btg(Id2): KAW556	Id2 Source: L	Nr Sus:	
	Breed: BL	Nr Pos:	
	Sex: M		
Ind Range:	Id3:	Pay Group:	Origin: C0555011 Q
Unit:	Id4:	Ind Id:	Origin State: CO
Nr In Lot:	Tat:	Case Nr:	Prem Name: Shulton Enterprises
	Id6:		Disposition:
OWNER INFORMATION			
Prem Id: Q		User Field 1:	L
Owner Name:		User Field 2:	L
Owner City:	Owner State:	User Field 3:	L
Owner Country:	County Name:		
Remarks:			
Test Name:			L
Test Result:			L

Summary	New	Clear	Save	Exit
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2A.14 Press **F10** to commit the data shown on this **TBCF** full-size **Sample** form into the GDB. You should always commit each individual **Sample** form's data before you start working in any other form.

You now have a **TBCF Sample Record** associated with the **TBCF Event_Summary Record** you created earlier in Exercise 1 of this lesson.

2A.15 You can now do any of the following:

To Start This Task...	Do This Action
Return to the TBCF Event_Summary form...	Either click the [Summary] command button or press CTRL+PAGE UP.
Start entering TBCF test results into this TBCF full-size Sample Record ... (Note: It is extremely rare that you will need to do this task. The test result for an animal's TBCF test is either P or N and will be exactly the same as the value already displayed in the Test_Interp field on the TBCF Sample form.)	Go directly to Step 2A.16 now.
Create a second TBCF Sample Record using the full-size Sample form...	Go directly to Step 2A.18 now.

2A.16 The *Test Information* block at the bottom of the form is linked to the **TBCF Sample Record** by the **TB Seq Nr** value shown in the *Sample Information* block.

To enter test results do the following:

- With your pointer in a field in the *Sample* block, press CTRL+PAGE DOWN (or simply click in the top-left **Test Name** field).

If default test values exist for the disease and species, these values will already appear in the **Test Name** and **Test Result** fields.
- Enter your new data or modify the default test data. Press ENTER to move the cursor between the **Test Name** and **Test Result** fields. Press DOWN ARROW or UP ARROW to move the cursor from one **Test Name** field to another **Test Name** field.

Below is an example of a completed *Test Information* block on a **TBCF** full-size **Sample** form:

Test Name: INS

Test Result: P

- Press **F10** to commit these test results data into the GDB.

An example of a completed **TBCF** full-size **Sample** form appears below:

SUMMARY INFORMATION			
TB Nr: 20031892665	Prem Id: C0988888	Prem State: CO	
Entry State: GA	Disease: TB	Species: BOV	
		Event Type: TBCF	

SAMPLE INFORMATION			
TB Seq Nr: 1	Eartag(Id1): GBB7209	Id1 Source: L	Age: 4
Bngl/Btg(Id2): WKA556	Id2 Source: L	Breed: BL	Test Interp: N
	Tag Query	Sex: M	Nr Neg:
			Nr Sus:
			Nr Pos:
Ind Range: I	Id3:	Pay Group: 7	Origin: C0988888
Unit:	Id4:	Ind Id:	Origin State: CO
Nr In Lot: 88	Tat:	Case Nr:	Prem Name: Maprin James R
	Id6:		Disposition:
OWNER INFORMATION			
Prem Id:	Owner Name:	Owner State:	User Field 1: L
Owner City:	Owner County:	County Name:	User Field 2: L
			User Field 3: L
Remarks:			
Test Name: INS			
Test Result: P			

Summary	New	Clear	Save	Exit
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2A.17 You can now do any of the following:

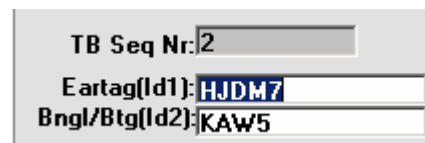
To Start This Task...	Do This Action
Create a second TBCF Sample Record using the full-size Sample form...	<ol style="list-style-type: none"> 1. Return the cursor to the <i>Sample Information</i> block either by pressing CTRL+PAGE UP. 2. Go directly to Step 2A.18 now.
Exit this TBCF full-size Sample form (because you have finished all of your data-entry work)...	<p>Click on the [Exit] command button.</p> <p>You have now finished this exercise.</p>

2A.18 The cursor should be in any field in the *Sample Information* block. Press **F6** or click the [New] button at the bottom of the form to start a new **TBCF** full-size **Sample** form.

Some fields will be cleared of their data; other fields will show new default values in them. And the cursor will move to the **TB Seq Nr** field, whose value will increase by one.

2A.19 Press ENTER to move the cursor to the **Eartag (Id1)** field.

2A.20 In the **Eartag (Id1)** field, the first five characters from the previous eartag number will be highlighted (as shown).



TB Seq Nr:	2
Eartag(Id1):	HJDM7
Bngl/Btg(Id2):	KAW5

If your next eartag starts with:

- *the same five characters*, press RIGHT ARROW. The cursor will move to the end of the highlighted characters. Finish entering the eartag number for the second animal in the sequence, if available.
- *different characters*, type the entire new number. Do not press the RIGHT ARROW key.
- *nothing* (because you do not have a second eartag number to report), press the [Delete] key on your keyboard.

Press ENTER to move the cursor to the **Bngl/Btg (Id2)** field.

2A.21 In the **Bngl/Btg (Id2)** field, the first four characters from the previous backtag number will be highlighted. (See the screen image earlier in Step 2A.20.)

If the next backtag starts with:

- *the same four characters*, press RIGHT ARROW. The cursor will move to the end of the highlighted characters. Finish entering the backtag number for the second animal in the sequence, if available.
- *different characters*, type the entire new number. Do not press the RIGHT ARROW key.
- *nothing* (because you do not have a second backtag number to report), press the [Delete] key on your keyboard.

Press ENTER to move the cursor to the **Age** field.

2A.22 In this step, you can enter new data or modify any default values shown in any field in the *Sample Information* block.

2A.23 After you have made any needed changes, press **F10** to commit the data on this **TBCF** full-size **Sample** form into the GDB.

2A.24 You can now do any of the following:

To Start This Task...	Do This Action
<p>Return to the TBCF Event_Summary form...</p> <p>Once you are back in the TBCF Event_Summary form, you can:</p> <ul style="list-style-type: none"> • Start another TBCF Event_Summary Record for a different premises... • Exit this form... 	<p>Either click the [Summary] command button or press CTRL+PAGE UP.</p> <p>→ Go directly now to <i>Exercise 3: Creating Additional TBCF Event_Summary Records</i> found in this lesson.</p> <p>→ Press CTRL+Q or the [Exit] command. You have now finished this Lesson 11.</p>
<p>Start entering TBCF test results into this second TBCF full-size Sample form...</p> <p>(Note: It is extremely rare that you will need to do this task. The test result for an animal's TBCF test is either P or N and will be exactly the same as the value already displayed in the Test_Interp field on the TBCF Sample form.)</p>	<p>Repeat Step 2A.16 earlier in this exercise.</p>
<p>Create additional TBCF Sample Records, using the full-size Sample form...</p>	<p>Repeat Steps 2A.18 – 2A.23 earlier in this exercise.</p>

Exercise 2B: Using the Short Sample Form

In this exercise, you will learn how to do enter TBCF animal sample data and test results data on a short **Sample** form.

- 2B.1 The cursor should still be inside any field in the *Event Summary Information* block of your **TBCF Summary** form. At the bottom of the form, click the [Short Sample] button.

A new **TBCF short Sample** form will appear:

SUMMARY INFORMATION									
ES NR	ST	Dis	Spe	Type	Date	Rsn	Seq NR		
20023571861	GA	TB	BOV	TBCF	04-OCT-2002	HQ	0		
Prem ID: C0555011		Prem Name: Shulton Enterprises				Prem State: CO			

SAMPLE INFORMATION														
Seq NR	I/R	Unit	NR in Lot	NR Neg	NR Sus	NR Pos	ID1 - Ear tag	ID2 - Backtag	ID5 - Vac	TI	Age	BR	Sex	Pay Grp
1										N				

Species: BOV
 Tag Query
 Origin: Q
 Origin State:
 Prem Name:

TEST INFORMATION										
Sample Seq NR: 1										
Test Name:										L
Test Result:										L

Summary
 New
 Clear
 Save
 Exit

Look at the *Sample Information* block. Each line (from the **Seq NR** field through the **Pay Grp** field) represents a separate **Sample** record. **Seq NR** is the only mandatory field in this block. But the more optional fields you complete, the more useful that record will be.

2B.2 Use the following guidelines to enter data in the *Sample Information* block of the **TBCF** short **Sample** form.

- The **Seq Nr** value (sequence number or tube number) can be changed.
- Use the **I/R** field to indicate whether the record applies to an individual (**I**) animal or a group (**R**) of animals.
 - If **I** is entered in this field, the record represents one animal. All ID information entered in the ID fields (**ID1**, **ID2**, and **ID5**) will pertain to one individual animal.
 - If **R** is entered in this field, the record represents a range of animals. The information entered in the ID fields will pertain to several animals.
- The **Unit** field may be used to record the lot number.

2B.3 After you finish creating the first **TBCF** short **Sample** record, press **F10** to commit it into the GDB.

Below is an example of a single **TBCF** short **Sample** record:

SAMPLE INFORMATION														Pay
Seq NR	I/R	Unit	NR in Lot	NR Neg	NR Sus	NR Pos	ID1 - Eartag	ID2 - Backtag	ID5 - Vac	TI	Age	BR	Sex	Grp
1							HJDM7209	KAW556		N	3	BL	M	

2B.4 To enter additional sample records on this **TBCF** short **Sample** form, do the following:

- a. Either click in the next blank field under **Seq NR** or press DOWN ARROW.
A **Seq Nr** value will appear there that is one higher than the previous **Seq NR**.
- b. Fill in the data fields as desired. Press ENTER or TAB to move from field to field.

- c. In the **ID1-Eartag** field, the first five characters from the previous eartag number will be displayed (as shown below).

SAMPLE INFORMATION														
Seq NR	I/R	Unit	NR in Lot	NR Neg	NR Sus	NR Pos	ID1 - Eartag	ID2 - Backtag	ID5 - Vac	TI	Age	BR	Sex	Pay Grp
1							HJDM7209	KAW556		N	3	BL	M	
2							HJDM7	KAW5		N	3	BL	M	

If your next eartag starts with:

- *the same five characters*, press RIGHT ARROW. The cursor will move to the end of the highlighted characters. Finish entering the eartag number for the second animal in the sequence, if available.
- *different characters*, type the entire new number. Do not press the RIGHT ARROW key.
- *nothing* (because you do not have a second eartag number to report), press the [Delete] key on your keyboard.

- d. In the **ID2-Backtag** field, the first four characters from the previous backtag number will be displayed. (See the screen image above.)

If the next backtag starts with

- *the same four characters*, press RIGHT ARROW. The cursor will move to the end of the highlighted characters. Finish entering the backtag number for the second animal in the sequence, if available.
 - *different characters*, type the entire new number. Do not press the RIGHT ARROW key.
 - *nothing* (because you do not have a second backtag number to report), press the [Delete] key on your keyboard.
- e. Modify any default values that were inserted into the current record from the previous record.
- f. Press **F10** to commit this second **TBCF** short **Sample** record into the GDB.
- g. Repeat Steps 2B.4a through 2B.4f for each additional **TBCF** short **Sample** record you need.

The example below of a completed **TBCF** short **Sample** form contains four animal sample records in it:

SAMPLE INFORMATION														Pay
Seq NR	I/R	Unit	NR in Lot	NR Neg	NR Sus	NR Pos	ID1 - Eartag	ID2 - Backtag	ID5 - Vac	TI	Age	BR	Sex	Grp
1							HJDM7209	KAW556		N	3	BL	M	
2							HJDM7210	KAW557		N	2	BL	F	
3							HJDM7211	KAW558		N	4	BL	M	
4							HJDM7212	KAW559		N	6	BL	M	

- 2B.5 Pressing the [Tag Query] button will cause the GDB to query its **Miscellaneous_Information Table** to find **Prem IDs** where tags were initially distributed.

(In order for this [Tag Query] button to work, the tag distribution information must already exist in the GDB's **Miscellaneous_Information Table**.)

- Any records retrieved will appear on a **Tag Distribution** form.
- You would then select the appropriate **Prem ID**.
- The **Prem ID** you select will be inserted into the **Origin** field of the **TBCF** short **Sample** form.

- 2B.6 If an animal came from another premises to the current premises, you can specify the original premises in the **Origin** sub-block.

Origin:	C0555011	Q
Origin State:	CO	
Prem Name:	Shulton Enterprises	

Enter a **Prem ID** value in the **Origin** field and press the **Q** button next to it.

A query will be executed against the GDB's **Premises Table**. If the **Prem ID** value in the **Origin** field matches a **Prem ID** in the **Premises Table**, the name of the premises that has this **Prem ID** will be displayed in the **Prem Name** field.

- 2B.7 Press **F10** to commit all of the data you have entered into the **TBCF** short **Sample** form. You now have one or more **TBCF** short **Sample** records associated with the **TBCF Event_Summary Record** you created earlier in Exercise 1 of this lesson.

Your **TBCF** short **Sample** record should look similar to the following:

SUMMARY INFORMATION																								
ES NR	ST	Dis	Spe	Type	Date	Rsn	Seq NR																	
20023571861	GA	TB	BOV	TBCF	04-OCT-2002	HQ	0																	
Prem ID: C0555011		Prem Name: Shulton Enterprises				Prem State: CO																		
SAMPLE INFORMATION																								
Seq NR	I/R	Unit	NR in Lot	NR Neg	NR Sus	NR Pos	ID1 - Eartag	ID2 - Backtag	ID5 - Vac	TI	Age	BR	Sex	Pay Grp										
1							HJDM7209	KAW556		N	3	BL	M											
2							HJDM7210	KAW557		N	2	BL	F											
3							HJDM7211	KAW558		N	4	BL	M											
4							HJDM7212	KAW559		N	6	BL	M											
Species: BOV												Tag Query												
Origin: C0555011												Q												
Origin State: CO																								
Prem Name: Shulton Enterprises																								
TEST INFORMATION																								
Sample Seq NR: 1																								
Test Name:																								
Test Result:																								
Summary					New					Clear					Save					Exit				

2B.8 You can now do any of the following:

To Start This Task...	Do This Action
Return to the TBCF Event_Summary form...	Either click the [Summary] command button or press CTRL+PAGE UP.
Start entering TBCF test results for this full-size Vaccination Sample Record ... (Note: It is extremely rare that you will need to do this task. The test result for an animal's TBCF test is either P or N and will be exactly the same as the value already displayed in the Test_Interp field on the TBCF Sample form.)	Go directly to Step 2B.9 below.

2B.9 To enter TBCF test results for a **TBCF** short **Sample** record, do the following:

- In the *Sample Information* block, click on the **Seq NR** value for the animal record whose test records you want to enter.
- Verify that this same value appears in both the *Sample Information* block's **Seq NR** field and in the *Test Information* block's **Sample Seq NR** field.

The example below shows that you will be entering test results for short **Sample Record #2** (indicated by the dark, heavy line).

SAMPLE INFORMATION														
Seq NR	I/R	Unit	NR in Lot	NR Neg	NR Sus	NR Pos	ID1 - Eartag	ID2 - Backtag	ID5 - Vac	TI	Age	BR	Sex	Pay Grp
1							HJDM7209	KAW556		N	3	BL	M	
2							HJDM7210	KAW557		N	2	BL	F	
3							HJDM7211	KAW558		N	4	BL	M	
4							HJDM7212	KAW559		N	6	BL	M	

Species: **BOV** Tag Query Origin: C0555011 Q
Origin State: CO Prem Name: Shulton Enterprises

TEST INFORMATION

Sample Seq NR: 2

Test Name: Test Result:

- c. Move the cursor down into the *Test Information* block by pressing CTRL+PAGE DOWN or clicking in the top **Test Name** field. Any existing default test values for your disease-species pair will already appear here. (Default test values are explained more fully in Lesson 3-Exercise 11 earlier in this manual.)

Within the *Test Information* block, press ENTER to move the cursor between the **Test Name** and **Test Result** fields. Press DOWN ARROW or UP ARROW to move the cursor from one **Test Name** field to another **Test Name** field.

Use the following guidelines to enter all of the test records that will apply to the animal indicated by the highlighted **Seq NR**:

- To enter a new value into a blank field, click in the field and type in your new data.
- To modify an existing test value, highlight the current value and type in your new value to replace it.
- To delete a default test record, move your cursor to the **Test Name** field containing the unwanted test. Press SHIFT+F6. This deletes the values from both the **Test Name** field and the **Test Result** field below it

- d. Press **F10** to commit the test results data into the GDB.

Below is an example of a **TBCF Test Results Record** for an animal whose **Sample Seq NR=2**. This record is displaying information for only one test, whose **Test Name=INS** and whose **Test Result=P**.

TEST INFORMATION

Sample Seq NR: 2

Test Name: INS Test Result: P

2B10. To enter test records for other animals whose **TBCF Sample Records** appear above in the *Sample Information* block, do the following:

- a. Press CTRL+PAGE UP to return to the *Sample Information* block.
- b. Repeat Step 2B.9.

2B.11 After you have created all of your animal **Sample Records** and their test records on the short **Sample** form, press **F10** to commit them into the GDB.

With the test records added, your completed **TBCF** short **Sample** form should now resemble the example shown below. In this example you can see:

SUMMARY INFORMATION									
ES NR	ST	Dis	Spe	Type	Date	Rsn	Seq NR		
20031892665	GA	TB	BOV	TBCF	12-OCT-2002	INSP	0		
Prem ID: C0988888		Prem Name: Maprin James R				Prem State: CO			

SAMPLE INFORMATION														
Seq NR	I/R	Unit	NR in Lot	NR Neg	NR Sus	NR Pos	ID1 - Eartag	ID2 - Backtag	ID5 - Vac	TI	Age	BR	Sex	Pay Grp
1	I						GBB7209	WKA556		N	4	BL	M	
2	I						GBB7210	WKA557		N	2	BL	F	
3	I						GBB7215	WKA561		N	3	BL	F	
4	I						GBB7218	WKA566		N	3	BL	M	

Species: BOV Tag Query Origin: C0988888 Q
 Origin State: CO
 Prem Name: Maprin James R

TEST INFORMATION												
Sample Seq NR: 2												
Test Name:	INS											L
Test Result:	P											L

Summary New Clear Save Exit

- four **TBCF** short **Sample Records** for four different animals.
- one **TBCF Test Results Record** for the animal whose **Seq NR=2**. (To view a test record for a different animal, click on that animal's **Seq NR** value up in the *Sample Information* block. Any test results attached to this **Seq NR** will automatically appear below in the *Test Information* block.) (Again, it is rare to see any test results displayed in a **TBCF Sample Record**; the example shown here is just to give you an idea.)

2B.12 Click the [Summary] button to return to the **TBCF Event_Summary** form. (You cannot use CTRL+PAGE UP in this form).

2B.13 You can now do any of the following:

To Start This Task...	Do This Action
Start a new TBCF Event_Summary Record for a different premises...	Go directly to <i>Exercise 3: Creating Additional TBCF Event_Summary Records</i> later in this lesson.
Exit this form (because you have finished all of your data-entry work)...	Click the [Exit] command button. You have now finished this Lesson 11.

Exercise 3: Creating Additional TBCF Event_Summary Records

- 3.1 To enter another **TBCF Event_Summary Record** for a different premises, return to the **TBCF Event_Summary** form. If you are in either the full-size or short **TBCF Sample** form, just click the [Summary] button at the bottom.

The cursor will appear in the **Disease** field of the *Event Summary Information* block on the **TBCF Event_Summary** form.

- 3.2 Start a new **TBCF Event_Summary** record by doing the following:
- Press CTRL+PAGE UP twice to place the cursor in the **Prem ID** field of the *Premises Query* block.
 - Press SHIFT+F7 to clear the fields in the *Premises Query* block.
 - Press **F7** to switch the form into data-retrieval mode.
 - In the **Prem ID** field, enter a new premises id.
 - Press **F8** to execute the query. If successful, the cursor will move down into the **Disease** field in the *Event Summary* block.
- 3.3 Enter your data in this new **TBCF Event_Summary** form by using the procedures already described back in Exercise 1 of this lesson.
- 3.4 To create any **TBCF Sample Records** and/or **TBCF Test Results Records** for this new **TBCF Event_Summary Record**, use the procedures described in Exercise 2 of this lesson.